PATENT

GISH et al.

Application No.: 09/930,020

Page 5

Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 4, at the end of the application.

REMARKS

Applicants request entry of this amendment in adherence with 37 C.F.R. §§1.821 to 1.825. This amendment is accompanied by a floppy disk containing the above named sequences, SEQ ID NOS:1-3, in computer readable form, and a paper copy of the sequence information which has been printed from the floppy disk.

The information contained in the computer readable disk was prepared through the use of the software program "PatentIn" and is identical to that of the paper copy. This amendment contains no new matter.

Attached hereto is a marked-up version of the changes made to the Specification and Abstract by the current Amendment. The attached pages are captioned "VERSION WITH MARKINGS TO SHOW CHANGES MADE."

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

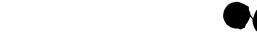
Respectfully submitted,

Reg. No. 34,774

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KLB:dmw





PATENT

GISH et al.

Application No.: 09/930,020

Page 6

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Paragraph [45] beginning at line 23 of page 6 has been amended as follows:

[45] The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. For example, cytokine receptors are characterized by a cluster of cysteines and a WSXWS (SEQ ID NO:3) (W= tryptophan, S= serine, X=any amino acid) motif. Immunoglobulin-like domains are highly conserved. Mucin-like domains may be involved in cell adhesion and leucine-rich repeats participate in protein-protein interactions.



GISH et al.

Application No.: 09/930,020

Page 7

Paragraph (TABLE 2) beginning at line 5 of page 96 has been amended as follows:

TABLE 2 CBF9 DNA and Protein Sequences

CBF9 DNA sequence (SEQ ID NO:1)

Gene name: ESTs
Unigene number: Hs.157601
Probeset Accession #: W07459
Nucleic Acid Accession #: AC005383

Coding Sequence: 328-2751 (underlined sequences correspond to start

and stop codons)

_						
1	11	21	31	41	51	
				1	<u> </u>	
				CGCGTAGAAG		60
			= '	CGAGGGGCTC		120
				GCCGCCCTCT		180
		GCAGCCGCGC				240
				GCCCGGGCAC		300
TCGCCGCTCT	CCTTCCGTTA	TATCAAC <u>ATG</u>	CCCCCTTTCC	TGTTGCTGGA	GGCCGTCTGT	360
GTTTTCCTGT				AGGAAGTCCA		420
GAAACCATCG	GGAAGATTTC	AGCTGCCAGC	AAAATGATGT	GGTGCTCGGC	TGCAGTGGAC	480
ATCATGTTTC	TGTTAGATGG	GTCTAACAGC	GTCGGGAAAG	GGAGCTTTGA	AAGGTCCAAG	540
CACTTTGCCA	TCACAGTCTG	TGACGGTCTG	GACATCAGCC	CCGAGAGGGT	CAGAGTGGGA	600
GCATTCCAGT	TCAGTTCCAC	TCCTCATCTG	GAATTCCCCT	TGGATTCATT	TTCAACCCAA	660
CAGGAAGTGA	AGGCAAGAAT	CAAGAGGATG	GTTTTCAAAG	GAGGGCGCAC	GGAGACGGAA	720
CTTGCTCTGA	AATACCTTCT	GCACAGAGGG	TTGCCTGGAG	GCAGAAATGC	TTCTGTGCCC	780
CAGATCCTCA	TCATCGTCAC	TGATGGGAAG	TCCCAGGGGG	ATGTGGCACT	GCCATCCAAG	840
CAGCTGAAGG	AAAGGGGTGT	CACTGTGTTT	GCTGTGGGGG	TCAGGTTTCC	CAGGTGGGAG	900
GAGCTGCATG	CACTGGCCAG	CGAGCCTAGA	GGGCAGCACG	TGCTGTTGGC	TGAGCAGGTG	960
GAGGATGCCA	CCAACGGCCT	CTTCAGCACC	CTCAGCAGCT	CGGCCATCTG	CTCCAGCGCC	1020
ACGCCAGACT	GCAGGGTCGA	GGCTCACCCC	TGTGAGCACA	GGACGCTGGA	GATGGTCCGG	1080
GAGTTCGCTG	GCAATGCCCC	ATGCTGGAGA	GGATCGCGGC	GGACCCTTGC	GGTGCTGGCT	1140
GCACACTGTC	CCTTCTACAG	CTGGAAGAGA	GTGTTCCTAA	CCCACCCTGC	CACCTGCTAC	1200
AGGACCACCT	GCCCAGGCCC	CTGTGACTCG	CAGCCCTGCC	AGAATGGAGG	CACATGTGTT	1260
CCAGAAGGAC	TGGACGGCTA	CCAGTGCCTC	TGCCCGCTGG	CCTTTGGAGG	GGAGGCTAAC	1320
TGTGCCCTGA	AGCTGAGCCT	GGAATGCAGG	GTCGACCTCC	TCTTCCTGCT	GGACAGCTCT	1380
GCGGGCACCA	CTCTGGACGG	CTTCCTGCGG	GCCAAAGTCT	TCGTGAAGCG	GTTTGTGCGG	1440
GCCGTGCTGA	GCGAGGACTC	TCGGGCCCGA	GTGGGTGTGG	CCACATACAG	CAGGGAGCTG	1500
CTGGTGGCGG	TGCCTGTGGG	GGAGTACCAG	GATGTGCCTG	ACCTGGTCTG	GAGCCTCGAT	1560
GGCATTCCCT	TCCGTGGTGG	CCCCACCCTG	ACGGGCAGTG	CCTTGCGGCA	GGCGGCAGAG	1620
CGTGGCTTCG	GGAGCGCCAC	CAGGACAGGC	CAGGACCGGC	CACGTAGAGT	GGTGGTTTTG	1680
CTCACTGAGT	CACACTCCGA	GGATGAGGTT	GCGGGCCCAG	CGCGTCACGC	AAGGGCGCGA	1740
GAGCTGCTCC	TGCTGGGTGT	AGGCAGTGAG	GCCGTGCGGG	CAGAGCTGGA	GGAGATCACA	1800
GGCAGCCCAA	AGCATGTGAT	GGTCTACTCG	GATCCTCAGG	ATCTGTTCAA	CCAAATCCCT	1860
GAGCTGCAGG	GGAAGCTGTG	CAGCCGGCAG	CGGCCAGGGT	GCCGGACACA	AGCCCTGGAC	1920
CTCGTCTTCA	TGTTGGACAC	CTCTGCCTCA	GTAGGGCCCG	AGAATTTTGC	TCAGATGCAG	1980
AGCTTTGTGA	GAAGCTGTGC	CCTCCAGTTT	GAGGTGAACC	CTGACGTGAC	ACAGGTCGGC	2040
		GGTGCAGACT		TGGACACCAA	ACCCACCCGG	2100
GCTGCGATGC	TGCGGGCCAT	TAGCCAGGCC	CCCTACCTAG	GTGGGGTGGG	CTCAGCCGGC	2160
				AGAGGGGTGC		2220



PATENT

GISH *et al.*Application No.: 09/930,020

Page 8

GTCCCCAAAG CTGTGGTGGT GCTCACAGGC GGGAGAGGCG CAGAGGATGC AGCCGTTCCT GCCCAGAAGC TGAGGAACAA TGGCATCTCT GTCTTGGTCG TGGGCGTGGG GCCTGTCCTA AGTGAGGGTC TGCGGAGGCT TGCAGGTCCC CGGGATTCCC TGATCCACGT GGCAGCTTAC GCCGACCTGC GGTACCACCA GGACGTGCTC ATTGAGTGGC TGTGTGGAGA AGCCAAGCAG CCAGTCAACC TCTGCAAACC CAGCCCGTGC ATGAATGAGG GCAGCTGCGT CCTGCAGAAT GGGAGCTACC GCTGCAAGTG TCGGGATGGC TGGGAGGGCC CCCACTGCGA GAACCGTGAG TGGAGCTCTT GCTCTGTATG TGTGAGCCAG GGATGGATTC TTGAGACGCC CCTGAGGCAC ATGGCTCCCG TGCAGGAGGG CAGCAGCCGT ACCCCTCCCA GCAACTACAG AGAAGGCCTG GGCACTGAAA TGGTGCCTAC CTTCTGGAAT GTCTGTGCCC CAGGTCCTTA GAATGTCTGC TTCCCGCCGT GGCCAGGACC ACTATTCTCA CTGAGGGAGG AGGATGTCCC AACTGCAGCC ATGCTGCTTA GAGACAAGAA AGCAGCTGAT GTCACCCACA AACGATGTTG TTGAAAAGTT TTGATGTGTA AGTAAATACC CACTTTCTGT ACCTGCTGTG CCTTGTTGAG GCTATGTCAT CTGCCACCTT TCCCTTGAGG ATAAACAAGG GGTCCTGAAG ACTTAAATTT AGCGGCCTGA CGTTCCTTTG CACACAATCA ATGCTCGCCA GAATGTTGTT GACACAGTAA TGCCCAGCAG AGGCCTTTAC TAGAGCATCC TTTGGACGGC GAAGGCCACG GCCTTTCAAG ATGGAAAGCA GCAGCTTTTC CACTTCCCCA GAGACATTCT GGATGCATTT GCATTGAGTC TGAAAGGGGG CTTGAGGGAC GTTTGTGACT TCTTGGCGAC TGCCTTTTGT GTGTGGAAGA GACTTGGAAA GGTCTCAGAC TGAATGTGAC CAATTAACCA GCTTGGTTGA TGATGGGGGA GGGGCTGAGT TGTGCATGGG CCCAGGTCTG GAGGGCCACG TAAAATCGTT CTGAGTCGTG AGCAGTGTCC 3360 ACCTTGAAGG TCTTC

CBF9 Protein sequence (SEO ID NO:2)

Gene name: ESTs Unigene number: Hs.157601

Protein Accession #: none found

Signal sequence: 1-17
Transmembrane domains: none found

VGW domains: 49-223; 341-518; 529-706

EGF domains: 298-333; 715-748 Cellular Localization: plasma membrane

1	11	21	31	41	51	
1			1	1		
MPPFLLLEAV	CVFLFSRVPP	SLPLQEVHVS	KETIGKISAA	SKMMWCSAAV	DIMFLLDGSN	60
SVGKGSFERS	KHFAITVCDG	LDISPERVRV	GAFQFSSTPH	LEFPLDSFST	QQEVKARIKR	120
MVFKGGRTET	ELALKYLLHR	GLPGGRNASV	PQILIIVTDG	KSQGDVALPS	KQLKERGVTV	180
FAVGVRFPRW	EELHALASEP	RGQHVLLAEQ	VEDATNGLFS	TLSSSAICSS	ATPDCRVEAH	240
PCEHRTLEMV	REFAGNAPCW	RGSRRTLAVL	AAHCPFYSWK	RVFLTHPATC	YRTTCPGPCD	300
SQPCQNGGTC	VPEGLDGYQC	LCPLAFGGEA	NCALKLSLEC	RVDLLFLLDS	SAGTTLDGFL	360
RAKVFVKRFV	RAVLSEDSRA	RVGVATYSRE	LLVAVPVGEY	QDVPDLVWSL	DGIPFRGGPT	420
	ERGFGSATRT					480
EAVRAELEEI	TGSPKHVMVY	SDPQDLFNQI	PELQGKLCSR	QRPGCRTQAL	DLVFMLDTSA	540
SVGPENFAQM	QSFVRSCALQ	FEVNPDVTQV	GLVVYGSQVQ	TAFGLDTKPT	RAAMLRAISQ	600
APYLGGVGSA	GTALLHIYDK	VMTVQRGARP	GVPKAVVVLT	GGRGAEDAAV	PAQKLRNNGI	660
SVLVVGVGPV	LSEGLRRLAG	PRDSLIHVAA	YADLRYHQDV	LIEWLCGEAK	QPVNLCKPSP	720
CMNEGSCVLQ	NGSYRCKCRD	GWEGPHCENR	EWSSCSVCVS	QGWILETPLR	HMAPVQEGSS	780
RTPPSNYREG	LGTEMVPTFW	NVCAPGP				